#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:37:42

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SEQUENCE LISTING
        1
        2
                   General Information:
        3
            (1)
                  (i) APPLICANT: Lyman, Stewart D.
                                 Beckmann, M. Patricia
        5
        6
        7
                 (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
        8
        9
                 (iii) NUMBER OF SEQUENCES: 8
       10
       11
                   (iv) CORRESPONDENCE ADDRESS:
                       (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
       12
                       (B) STREET: 51 University Street
       13
                       (C) CITY: Seattle
       14
                       (D) STATE: Washington
       15
                       (E) COUNTRY: US
       16
                       (F) ZIP: 98101
       17
       18
                 (v) COMPUTER READABLE FORM:
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                       (A) MEDIUM TYPE: Floppy disk
       20
                       (B) COMPUTER: Apple Macintosh
       21
                       (C) OPERATING SYSTEM: Macintosh 7.0.1
       22
       23
                       (D) SOFTWARE: Microsoft Word, Version #5.1
       24
       25
                (vi) CURRENT APPLICATION DATA:
                       (A) APPLICATION NUMBER: -to be assigned-
       26
       27
                       (B) FILING DATE: December 3, 1993
       28
                       (C) CLASSIFICATION:
       29
       30
               (vii) PRIOR APPLICATION DATA:
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                       (A) APPLICATION NUMBER: 08/111,758
                       (B) FILING DATE: August 25, 1993
       32
                       (C) CLASSIFICATION:
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                       (A) APPLICATION NUMBER: 08/106,463
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                       (B) FILING DATE: August 12, 1993
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                       (C) CLASSIFICATION:
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               (vii) PRIOR APPLICATION DATA:
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                       (A) APPLICATION NUMBER: 08/068,394
       42
                       (B) FILING DATE: May 24, 1993
       43
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                       (C) CLASSIFICATION:
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       45
              (viii) ATTORNEY/AGENT INFORMATION:
       46
                       (A) NAME: Malaska, Stephen L.
                       (B) REGISTRATION NUMBER: 32,655
       47
       48
                       (C) REFERENCE/DOCKET NUMBER: 2813-C
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       50
                (ix) TELECOMMUNICATION INFORMATION:
                       (A) TELEPHONE: (206) 587-0430
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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:37:48

52 53				B) T				) 23	3-06	44							
54 55 56	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:1	:								
57 58 59 60 61 62		(i)	(1	~	ENGTI YPE : IRANI	H: 8' nuc	79 ba leic ESS:	ase pacions	pair: d	S							
63 64		(ii	) MO	LECUI	LE T	YPE:	CDN	A to	mRN	A							
65 66		(iii)	) HY	POTH	ETIC	AL: 1	OV										
67 68		(iv	) AN	ri-si	ENSE	: NO											
69 70 71 72		(ix)			AME/I				atur	€							
73 74 75 76		(ix)			AME/I			_	ature 9	<b>e</b>							
77 78 79 80 81		(ix)		ATURI A) NI 3) L(	AME/I			. 752									
82 83		(xi)	) SE(	QUEN	CE DI	ESCR	IPTI	ON: S	SEQ I	ID NO	0:1:						
84 85	GTC	GACT(	GGA A	ACGA	GACG	AC C	rgcT(	CTGT	C AC	AGGC	ATGA	GGG	TCC	CCG (	GCAG!	AG	56
86 87 88 89															TTG Leu 15	CTG Leu	104
90 91 92				Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	TGT Cys	-	152
93 94 95				AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA Arg	GAG	200
96 97 98 99 100															GTC Val		248
101 102															CTA Leu		296

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:37:54

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105	CAG	CGC	TGG	АТА	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	тст	AAG	ATG	CAA	344
106															Met		
107			L	_	85					90		1		-1-	95		
108																	
109	ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	АТА	САТ	ттт	GTC	ACC	TCA	тст	392
110															Ser		332
111				100	E				105					110		070	
112																	
113	ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	440
114															Asn		
115			115					120		5			125				
116																	
117	TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	СТТ	GCT	CTG	AAG	CCC	488
118															Lys		
119		130			-7-		135	-7-				140			-1-		
120																	
121	TGT	ATC	GGG	AAG	GCC	TGC	CAG	AAT	TTC	тст	CGG	TGC	CTG	GAG	GTG	CAG	536
122															Val		
123	145		1	-1-		150					155	-7.				160	
124																	
125	TGC	CAG	CCG	GAC	TCC	TCC	ACC	CTG	CTG	CCC	CCA	AGG	AGT	CCC	ATA	GCC	584
126															Ile		501
127	-1-			E	165					170		5			175		
128																	
129	CTA	GAA	GCC	ACG	GAG	CTC	CCA	GAG	CCT	CGG	CCC	AGG	CAG	CTG	TTG	CTC	632
130															Leu		
131				180					185			,		190			
132																	
133	CTG	CTG	CTG	CTG	CTG	CCT	CTC	ACA	CTG	GTG	CTG	CTG	GCA	GCC	GCC	TGG	680
134	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp	
135			195					200					205			-	
136																	
137	GGC	CTT	CGC	TGG	CAA	AGG	GCA	AGA	AGG	AGG	GGG	GAG	CTC	CAC	CCT	GGG	728
138	Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly	
139	_	210	_	_		•	215	_	•	_	-	220				-	
140																	
141	GTG	CCC	CTC	CCC	TCC	CAT	CCC	TAGG	ATTO	GA G	CCTI	GTG	A TO	GTT	ACTO	2	779
142	Val	Pro	Leu	Pro	Ser	His	Pro										
143	225					230											
144																	
145	AGC	CAGGG	TC T	TATC	CTCGG	T T	CAC	TGT	ATC	TCAC	CCC	TTG	GAGO	CCC A	AGAGO	CAGGAT	839
146																	
147	TGCT	'GAA'	GG 1	CTG	AGCA	G GI	CGTC	TCGT	TCC	CAGTO	CGAC						879
148																	
149	(2)	INFO	RMAI	CION	FOR	SEQ	ID N	10:2:									
150																	
151		(	(i) S														
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153				(B)	TYE	PE: a	ıminc	aci	.d								

## RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:37:59

154	54 (D) TOPOLOGY: linear															
155	(ii) MOLECULE TYPE: protein															
156 157		(:	11) !	MOLE	COLE	TABI	E: p:	rote:	ın							
158																
159		(:	xi)	SEQUI	ENCE	DESC	CRIP'	TION	: SE	O ID	NO:	2:				
160				_					•	-						
161	Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu
162	1				5					10					15	
163			<b>-</b> .	_	_	•	_	_	_	_	~7		_	_	~	_
164 165	ьеи	ьeu	ьeu	ьеи 20	Leu	ser	Pro	Cys		Arg	GIY	Thr	Pro		Cys	Tyr
166				20					25					30		
167	Phe	Ser	His	Ser	Pro	Tle	Ser	Ser	Δsn	Dhe	Lvg	Val	Lva	Dhe	Arg	Glu
168	1110	501	35	001	0	110	501	40	21011	1110	טעם	val	45	1110	****9	014
169																
170	Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn
171		50	_				55	_	-			60				
172																
173		Gln	Asp	Glu	Lys		Cys	Lys	Ala	Leu		Ser	Leu	Phe	Leu	
174	65					70					75					80
175 176	Cln.	7 ~~	Two	T10	C1	Cln	T 011	Tvra		7707	71-	C1	Cox	Trra	Mot	C1 5
177	GIII	Arg	пр	TTE	85	GIII	ьeu	гуя	TILL	90	Ата	GIY	ser	гуѕ	Met 95	GIII
178					0,5					90					93	
179	Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cvs
180				100					105					110		-1
181																
182	Thr	Phe	${\tt Gln}$	Pro	Leu	${\tt Pro}$	Glu	Cys	Leu	Arg	Phe	Val	${\tt Gln}$	Thr	Asn	Ile
183			115					120					125			
184	_		_	_	_	_		_			_	_		_	_	_
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186 187		130					135					140				
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189	145		0-1	_,5		150	0111	11011		001	155	Cyb		014	V41	160
190																
191	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala
192					165					170					175	
193																
194	Leu	Glu	Ala		Glu	Leu	Pro	Glu		Arg	Pro	Arg	Gln		Leu	Leu
195				180					185					190		
196 197	Lou	T.011	Len	Lou	T.011	Dro	Lou	Thr	Lou	17-1	Lou	Lou	7 7 -	712	Ala	Trn
198	ьeu	пеп	195	пеп	пеп	PIO	ьеu	200	пеп	val	Беп	ьеи	205	AIA	АІА	пр
199			175					200					203			
200	Gly	Leu	Arq	Trp	Gln	Arq	Ala	Arq	Arq	Arq	Gly	Glu	Leu	His	Pro	Gly
201	•	210	_	-		_	215	_	_		-	220				-
202																
203		Pro	Leu	Pro	Ser	-	Pro									
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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:04

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A		/ + \	CECTENCE CUADACTEDICTICS.	
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213 214 (iii) HYPOTHETICAL: NO 215 216 (iv) ANTI-SENSE: NO 217 218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 219 220 TCGACTGGAA CGAGACGACC TGCT 24 221 222 223 (2) INFORMATION FOR SEQ ID NO:4: 224 225 (i) SEQUENCE CHARACTERISTICS: 226 (a) LENGTH: 20 base pairs 227 (B) TYPE: nucleic acid 228 (C) STRANDEDNESS: single 229 (D) TOPOLOGY: linear 230 231 (iii) HYPOTHETICAL: NO 232 233 (iv) ANTI-SENSE: NO 234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 236 237 AGCAGGTCGT CTCGTTCCAG 20 238 239 (2) INFORMATION FOR SEQ ID NO:5: 240 (i) SEQUENCE CHARACTERISTICS: 241 (i) SEQUENCE CHARACTERISTICS: 242 (A) LENGTH: 988 base pairs 243 (B) TYPE: nucleic acid 244 (C) STRANDEDNESS: single 245 (D) TOPOLOGY: linear 246 247 (ii) MOLECULE TYPE: cDNA to mRNA 248 249 (iii) HYPOTHETICAL: NO 250 251 (iv) ANTI-SENSE: NO 252 253 (ix) FEATURE: 254 (A) NAME/KEY: CDS				
11			(D) TOPOLOGI: IIIIeal	
215 216 (iv) ANTI-SENSE: NO 217 218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 219 220 TCGACTGGAA CGAGACGACC TGCT 24 221 222 223 (2) INFORMATION FOR SEQ ID NO:4: 224 225 (i) SEQUENCE CHARACTERISTICS: 226 (A) LENGTH: 20 base pairs 227 (B) TYPE: nucleic acid 228 (C) STRANDEDNESS: single 229 (D) TOPOLOGY: linear 230 231 (iii) HYPOTHETICAL: NO 232 233 (iv) ANTI-SENSE: NO 234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 236 AGCAGGTCGT CTCGTTCCAG 20 237 AGCAGGTCGT CTCAGTTCCAG 20 240 (i) SEQUENCE CHARACTERISTICS: 241 (i) SEQUENCE CHARACTERISTICS: 242 (A) LENGTH: 988 base pairs 243 (B) TYPE: nucleic acid 244 (C) STRANDEDNESS: single 245 (D) TOPOLOGY: linear 246 (ii) MOLECULE TYPE: cDNA to mRNA 247 (ii) MOLECULE TYPE: cDNA to mRNA 248 (iii) HYPOTHETICAL: NO 250 (iv) ANTI-SENSE: NO 251 (iv) ANTI-SENSE: NO 252 (ix) FEATURE: 253 (ix) FEATURE: 254 (A) NAME/KEY: CDS		1:::1	INDOMIETICAL. NO	
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18		(10)	ANII-SENSE: NO	
219 220		(2ci)	CECTENCE DECEDIDATION. CEC ID NO.2.	
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221 222 223 224 225 226 227 228 226 227 228 227 228 227 228 228 229 230 231 230 231 231 231 232 233 231 232 233 233 240 234 235 236 237 240 238 239 230 231 230 231 231 231 232 233 233 231 234 235 237 240 241 255 261 27 282 283 29 29 20 20 20 20 20 20 20 21 20 21 22 23 23 24 25 26 27 28 28 29 29 20 20 20 20 21 21 22 23 23 24 25 26 27 28 29 20 20 21 20 21 21 22 22 23 23 24 25 26 27 28 29 20 20 21 21 22 22 23 23 24 25 26 27 28 29 29 20 20 21 21 22 22 23 23 24 25 26 27 28 29 29 20 20 21 21 22 23 24 24 25 26 26 27 28 28 29 29 20 20 21 21 22 23 23 24 24 25 26 26 27 28 28 29 29 20 20 20 21 21 22 23 24 24 25 26 26 27 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20		ጥሮሮን ሮሞሮሮ	AA CCACACCACC TCCT	24
222 223 (2) INFORMATION FOR SEQ ID NO:4:  224 225 (i) SEQUENCE CHARACTERISTICS: 226 (A) LENGTH: 20 base pairs 227 (B) TYPE: nucleic acid 228 (C) STRANDEDNESS: single 229 (D) TOPOLOGY: linear  230 231 (iii) HYPOTHETICAL: NO  232 233 (iv) ANTI-SENSE: NO  234 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  236 237 AGCAGGTCGT CTCGTTCCAG 20 238 239 (2) INFORMATION FOR SEQ ID NO:5:  240 (i) SEQUENCE CHARACTERISTICS: 241 (i) SEQUENCE CHARACTERISTICS: 242 (A) LENGTH: 988 base pairs 243 (B) TYPE: nucleic acid 244 (C) STRANDEDNESS: single 245 (D) TOPOLOGY: linear  246 247 (ii) MOLECULE TYPE: cDNA to mRNA  248 249 (iii) HYPOTHETICAL: NO  251 (iv) ANTI-SENSE: NO  252 253 (ix) FEATURE: 254 (A) NAME/KEY: CDS		ICGACIGG	AA CGAGACGACC IGCI	24
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230 231 (iii) HYPOTHETICAL: NO 232 233 (iv) ANTI-SENSE: NO 234 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 236 237 AGCAGGTCGT CTCGTTCCAG 20 238 239 (2) INFORMATION FOR SEQ ID NO:5: 240 241 (i) SEQUENCE CHARACTERISTICS: 242 (A) LENGTH: 988 base pairs 243 (B) TYPE: nucleic acid 244 (C) STRANDEDNESS: single 245 (D) TOPOLOGY: linear 246 247 (ii) MOLECULE TYPE: cDNA to mRNA 248 249 (iii) HYPOTHETICAL: NO 250 251 (iv) ANTI-SENSE: NO 252 253 (ix) FEATURE: 254 (A) NAME/KEY: CDS				
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245 (D) TOPOLOGY: linear 246 247 (ii) MOLECULE TYPE: cDNA to mRNA 248 249 (iii) HYPOTHETICAL: NO 250 251 (iv) ANTI-SENSE: NO 252 253 (ix) FEATURE: 254 (A) NAME/KEY: CDS	243		(B) TYPE: nucleic acid	
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		(ix)	FEATURE:	
255 (B) LOCATION: 30734			·	
	255		(B) LOCATION: 30734	

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

INPUT SET: S1194.raw

DATE: 12/27/93 TIME: 12:38:10

256 257		(xi	) SE	QUEN	CE DI	ESCR	IPTIO	ON: S	SEQ :	ID NO	0:5:				
258 259 260 261 262	CGG	CCGG	AAT '	rccg(	GGGC(	CC C	CGGC	CGAA					CCA Pro		53
263 264 265 266			ACA Thr												101
267 268 269 270			ACC Thr												149
271 272 273 274			GTC Val												197
275 276 277 278			ACC Thr												245
279 280 281 282			CGG Arg 75												293
283 284 285 286			GGG Gly											GAG Glu	341
287 288 289 290			TTT Phe												389
291 292 293 294			GTC Val												437
295 296 297 298			GTG Val												485
299 300 301			GAG Glu 155												533
302 303 304 305 306			CCC Pro												581

## RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:15

307	CCT CTG	CTC	CTC	CTA	CTG	CTG	CTG	CCC	GTG	GGC	CTC	CTG	CTG	CTG	GCC	629
308	Pro Leu	Leu	Leu	Leu		Leu	Leu	Pro	Val	-	Leu	Leu	Leu	Leu		
309 310	185				190					195					200	
311	GCT GCC	TGG	TGC	CTG	CAC	TGG	CAG	AGG	ACG	CGG	CGG	AGG	ACA	CCC	CGC	677
312	Ala Ala															
313				205					210					215		
314																
315 316	CCT GGG															725
317	Pro Gly	GIU	220	vai	PIO	PIO	vai	225	ser	PIO	GIII	Asp	230	ьeu	Leu	
318			220					223					250			
319	GTG GAG	CAC	TGAC	CCTG	GCC I	AAGG	CCTC	AT CO	CTGC	GAG	CT	CAAA	CAAC		•	774
320	Val Glu	His														
321		235														
322																
323	GCAGTGA	GAC A	GAC	ATCT	AT C	ATCC	CATT!	TAC	CAGG	GAG	GAT	ACTG	AGG (	CACAC	CAGAGG	834
324 325	GGAGTCA	ממא מ	יממאמ	מא מכני	ייי כיי	ר איזי איז	יי רי ריידי	י מאני	יאריאר	מאממ	אאפי	PTPCC/C	מיחיר (	בא כיכי	тесете	001
326	GGAGICA	CCA G	CCAC	ADDAC	11 G.	IAIA	30010	J GAG	-ACA(	DAGG	AAG.	11660	JIA	DODAE	LCGGIC	034
327	CCTTCCT	TGG G	CCCC	стстс	CA T	rccc1	rccc	AG	AATGO	AGG	CAA	CGCCZ	AGA A	ATCC	AGCACC	954
328																
329	GGCCCCA	TTT A	CCCF	ACTO	CT GA	AACA	AAGC	CCC	CG							988
330																
331	(2) INF	ORMAT	'ION	FOR	SEQ	ID 1	10:6	:								
332		(i) c	EOI II	יאורים:	CHVE	ን አ ረግጥ፤	יסדפי	ידרפ.	-							
333		(i) s	~													
		(i) S	(A)	ENCE LEN	IGTH :	235	5 ami	.no a		3						
333 334		(i) S	(A) (B)	LEN	NGTH:	: 235 amino	ā ami	.no a .d		3						
333 334 335 336 337			(A) (B) (D)	LEN TYI TOI	IGTH: PE: & POLOG	: 235 amino 3Y: ]	ami aci linea	.no a .d ır		3						
333 334 335 336 337 338		(i) S ii) M	(A) (B) (D)	LEN TYI TOI	IGTH: PE: & POLOG	: 235 amino 3Y: ]	ami aci linea	.no a .d ır		3						
333 334 335 336 337 338 339	(	ii) M	(A) (B) (D)	LEN TYP TOP	NGTH: PE: & POLOG TYPE	: 235 amino 3Y: ] E: pr	ami aci linea cotei	.no a .d .r .n	acids							
333 334 335 336 337 338 339 340	(		(A) (B) (D)	LEN TYP TOP	NGTH: PE: & POLOG TYPE	: 235 amino 3Y: ] E: pr	ami aci linea cotei	.no a .d .r .n	acids		5:					
333 334 335 336 337 338 339	(:	ii) M xi) S	(A) (B) (D) (OLEC	LENTY TO I	OTH:	: 235 amino EY: ] E: pr	ami o aci linea cotei	no a d ir n seç	acids	NO : 6		Tvr	Leu	Leu	Leu	
333 334 335 336 337 338 339 340 341	(	ii) M xi) S	(A) (B) (D) (OLEC	LENTY TO I	OTH:	: 235 amino EY: ] E: pr	ami o aci linea cotei	no a d ir n seç	acids	NO : 6		Tyr	Leu	Leu 15	Leu	
333 334 335 336 337 338 339 340 341 342	( (: Met Thr	ii) M xi) S	(A) (B) (D) (OLEC	LEN TYPE TOPE CULE ENCE	OGTH: PE: 6 POLOC TYPE DESC	: 235 amino EY: ] E: pr	ami o aci linea cotei	no a d ir n seç	acids	NO : 6		Tyr	Leu		Leu	
333 334 335 336 337 338 339 340 341 342 343 344 345	( (: Met Thr	ii) M xi) S Val	(A) (B) (D) (OLEC EQUE Leu	LEN TYI TOI CULE ENCE Ala 5	GTH: PE: a POLOG  TYPE  DESG  Pro	: 235 amino GY: ] E: pr CRIPT	ami o aci linea rotei rion:	no a d ir n SE( Ser	Q ID Pro 10	NO:6	Thr	_	Cys	15		
333 334 335 336 337 338 339 340 341 342 343 344 345 346	( (: Met Thr 1	ii) M xi) S Val	(A) (B) (D) (OLEC EQUE	LEN TYI TOI CULE ENCE Ala 5	GTH: PE: a POLOG  TYPE  DESG  Pro	: 235 amino GY: ] E: pr CRIPT	ami o aci linea rotei rion:	no a d ir n SE(	Q ID Pro 10	NO:6	Thr	_		15		
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347	( (: Met Thr 1 Leu Leu	ii) M xi) S Val Leu	(A) (B) (D) (OLEC EQUE Leu Leu 20	TYPETULE ENCE Ala 5	TYPE DESC	: 235 amino GY: ]  CRIPT Ala  Gly	o ami o aci linea rotei rion: Trp	no a d ir n SEQ Ser Ser	Pro 10	NO:6	Thr Gln	Asp	Cys 30	15 Ser	Phe	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348	( (: Met Thr 1	ii) M xi) S Val Leu Ser	(A) (B) (D) (OLEC EQUE Leu Leu 20	TYPETULE ENCE Ala 5	TYPE DESC	: 235 amino GY: ]  CRIPT Ala  Gly	amic aci linea rotei TION: Trp Leu	no a d ir n SEQ Ser Ser	Pro 10	NO:6	Thr Gln	Asp	Cys 30	15 Ser	Phe	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347	( (: Met Thr 1 Leu Leu	ii) M xi) S Val Leu	(A) (B) (D) (OLEC EQUE Leu Leu 20	TYPETULE ENCE Ala 5	TYPE DESC	: 235 amino GY: ]  CRIPT Ala  Gly	o ami o aci linea rotei rion: Trp	no a d ir n SEQ Ser Ser	Pro 10	NO:6	Thr Gln	Asp	Cys 30	15 Ser	Phe	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351	( (: Met Thr 1 Leu Leu	ii) M xi) S Val Leu Ser 35	(A) (B) (D) (OLEC EQUE Leu 20 Pro	LENTYI TOI CULE ENCE Ala 5 Ser	TYPE DESC Pro Ser	: 235 amino GY: ] E: pr CRIPT Ala Gly Ser	E ami D aci D aci Linea COTEI TION: Trp Leu Asp 40	no a d ir .n SE( Ser 25 Phe	Q ID Pro 10 Gly	NO:6 Thr Thr	Thr Gln Lys	Asp Ile 45	Cys 30 Arg	15 Ser Glu	Phe Leu	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352	(()  Met Thr  1  Leu Leu  Gln His	ii) M xi) S Val Leu Ser 35	(A) (B) (D) (OLEC EQUE Leu 20 Pro	LENTYI TOI CULE ENCE Ala 5 Ser	TYPE DESC Pro Ser	: 235 amino GY: ] E: pr CRIPT Ala Gly Ser	E ami D aci D aci Linea COTEI TION: Trp Leu Asp 40	no a d ir .n SE( Ser 25 Phe	Q ID Pro 10 Gly	NO:6 Thr Thr	Thr Gln Lys	Asp Ile 45	Cys 30 Arg	15 Ser Glu	Phe Leu	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353	Met Thr 1 Leu Leu Gln His Ser Asp	ii) M xi) S Val Leu Ser 35	(A) (B) (D) (OLEC EQUE Leu 20 Pro	LENTYI TOI CULE ENCE Ala 5 Ser Ile Leu	TYPE DESC Pro Ser Ser	E: 235 Amino GY: ] CRIPT Ala Gly Ser Asp 55	Trp  Leu  Asp 40	no and and ar and ar	Pro 10 Gly Ala	NO:6 Thr Thr Val	Thr Gln Lys Val	Asp Ile 45 Ala	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354	Met Thr 1 Leu Leu Gln His Ser Asp 50 Gln Asp	ii) M xi) S Val Leu Ser 35	(A) (B) (D) (OLEC EQUE Leu 20 Pro	LENTYI TOI CULE ENCE Ala 5 Ser Ile Leu	GTH: PE: a POLOG  TYPE  DESG  Pro  Ser  Ser  Gln  Cys	E: 235 Amino GY: ] CRIPT Ala Gly Ser Asp 55	Trp  Leu  Asp 40	no and and ar and ar	Pro 10 Gly Ala	NO:6 Thr Thr Val Thr Arg	Thr Gln Lys Val	Asp Ile 45 Ala	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu Gln	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355	Met Thr 1 Leu Leu Gln His Ser Asp	ii) M xi) S Val Leu Ser 35	(A) (B) (D) (OLEC EQUE Leu 20 Pro	LENTYI TOI CULE ENCE Ala 5 Ser Ile Leu	TYPE DESC Pro Ser Ser	E: 235 Amino GY: ] CRIPT Ala Gly Ser Asp 55	Trp  Leu  Asp 40	no and and ar and ar	Pro 10 Gly Ala	NO:6 Thr Thr Val	Thr Gln Lys Val	Asp Ile 45 Ala	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354	Met Thr 1 Leu Leu Gln His Ser Asp 50 Gln Asp	ii) M xi) S Val Leu Ser 35 Tyr	(A) (B) (D) (OLEC EQUE Leu 20 Pro Leu Glu	LENTYI TOI CULE ENCE Ala 5 Ser Ile Leu Leu	TYPE DESC Pro Ser Gln Cys 70	E: 235 Amino CY: 1 CRIPT Ala Gly Ser Asp 55	Trp  Leu  Asp 40  Tyr	no and and ar and ar	Pro 10 Gly Ala Val	NO:6 Thr Thr Val Thr Arg 75	Thr Gln Lys Val 60 Leu	Asp Ile 45 Ala Val	Cys 30 Arg Ser	15 Ser Glu Asn Ala	Phe Leu Leu Gln 80	

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:20

358 359					85					90					95		
360 361 362	Leu	Leu	Glu	Arg 100	Val	Asn	Thr	Glu	Ile 105	His	Phe	Val	Thr	Lys 110	Cys	Ala	
363 364 365	Phe	Gln	Pro 115	Pro	Pro	Ser	Cys	Leu 120	Arg	Phe	Val	Gln	Thr 125	Asn	Ile	Ser	
366 367 368	Arg	Leu 130	Leu	Gln	Glu	Thr	Ser 135	Glu	Gln	Leu	Val	Ala 140	Leu	Lys	Pro	Trp	
369 370 371	Ile 145	Thr	Arg	Gln	Asn	Phe 150	Ser	Arg	Cys	Leu	Glu 155	Leu	Gln	Cys	Gln	Pro 160	
372 373 374	Asp	Ser	Ser	Thr	Leu 165	Pro	Pro	Pro	Trp	Ser 170	Pro	Arg	Pro	Leu	Glu 175	Ala	
375 376 377	Thr	Ala	Pro	Thr 180	Ala	Pro	Gln	Pro	Pro 185	Leu	Leu	Leu	Leu	Leu 190	Leu	Leu	
378 379 380	Pro	Val	Gly 195	Leu	Leu	Leu	Leu	Ala 200	Ala	Ala	Trp	Cys	Leu 205	His	Trp	Gln	
381 382 383	Arg	Thr 210	Arg	Arg	Arg	Thr	Pro 215	Arg	Pro	Gly	Glu	Gln 220	Val	Pro	Pro	Val	
384 385 386	Pro 225	Ser	Pro	Gln	Asp	Leu 230	Leu	Leu	Val	Glu	His 235						
387 388	(2)	INFO	ORMA'	NOI	FOR	SEQ	ID 1	NO : 7 :	:								
389 390 391 392 393 394		(i)	( <i>I</i> (I	A) LE 3) TY C) ST	ENGTI (PE :   RANI	i: 71	l bas Leic ESS:	ISTIC se pa ació sing ear	airs 1								
395 396		(ii)	MOI	LECUI	E TY	PE:	cDNA	A to	mRNA	Ą							
397 398	•	(iii)	HYI	POTHE	ETICA	AL: 1	10										
399 400 401 402 403		(iv)	ANT	TI-SE	ENSE :	NO											
404 405		(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ I	D NO	):7:						
406 407	AATT	rggt <i>f</i>	ACC I	TTGG	ATA	AA AG	BAGAC	CTACA	A AGG	ACGA	ACGA	TGAC	CAAGA	ACA (	CTGA	CTGTT	60
408	ACTT	CAGC	CA C	2													71

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:26

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415	(C) STRANDEDNESS: single	
416	(D) TOPOLOGY: linear	
417		
418	(ii) MOLECULE TYPE: cDNA to mRNA	
419	4444	
420	(iii) HYPOTHETICAL: NO	
421	(1.)	
422	(iv) ANTI-SENSE: NO	
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424		
425		
426	(-1) GROWING DECERTIFIED GEO. ID NO. 0	
427	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
428		37
429 <sup>1</sup>	ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG	3 /
430		
431		
432	·	
433		

# SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:29

Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: -to be assigned-
33 38	Unknown or Misplaced Identifier Unknown or Misplaced Identifier	(C) CLASSIFICATION: (C) CLASSIFICATION:
43	Unknown or Misplaced Identifier	(C) CLASSIFICATION:

## SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:29

INPUT SET: S1194.raw

<< THERE ARE NO ITEMS MISSING >>

## SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/162,407

DATE: 12/27/93 TIME: 12:38:30

INPUT SET: S1194.raw

Line

Original Text

Corrected Text